

Andres

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TECH CENTER 1600/2300

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/423,943

DATE: 09/26/2000
 TIME: 16:40:05

Input Set : A:\Cbm-70wo.app
 Output Set: N:\CRF3\09262000\I423943.raw

3 <110> APPLICANT: Sampath, Kuber T.
 4 Cohen, Charles M.
 6 <120> TITLE OF INVENTION: Methods For Tissue Morphogenesis and Methods for
 7 Evaluating Morphogenic Activity
 9 <130> FILE REFERENCE: Seq. Listing For CBM-70 WO
 11 <140> CURRENT APPLICATION NUMBER: 09/423943
 C--> 12 <141> CURRENT FILING DATE: 2000-03-18
 14 <160> NUMBER OF SEQ ID NOS: 9
 16 <170> SOFTWARE: PatentIn Ver. 2.0
 18 <210> SEQ ID NO: 1
 19 <211> LENGTH: 1822
 20 <212> TYPE: DNA
 21 <213> ORGANISM: Homo sapiens
 23 <220> FEATURE:
 24 <221> NAME/KEY: CDS
 25 <222> LOCATION: (49)..(1341)
 26 <223> OTHER INFORMATION: "Morphogenic Protein OP-1"
 28 <400> SEQUENCE: 1
 29 ggtgcgggcc cggagcccg agcccggtg gcgcgtagag ccggcgcg atg cac gtg 57
 30 Met His Val
 31 1
 33 cgc tca ctg cga gct gcg gcg ccg cac agc ttc gtg gcg ctc tgg gca 105
 34 Arg Ser Leu Arg Ala Ala Ala Pro His Ser Phe Val Ala Leu Trp Ala
 35 5 10 15
 37 ccc ctg ttc ctg ctg cgc tcc gcc ctg gcc gac ttc agc ctg gac aac 153
 38 Pro Leu Phe Leu Leu Arg Ser Ala Leu Ala Asp Phe Ser Leu Asp Asn
 39 20 25 30 35
 41 gag gtg cac tcg agc ttc atc cac cgg cgc ctc cgc agc cag gag cgg 201
 42 Glu Val His Ser Ser Phe Ile His Arg Arg Leu Arg Ser Gln Glu Arg
 43 40 45 50
 45 cgg gag atg cag cgc gag atc ctc tcc att ttg ggc ttg ccc cac cgc 249
 46 Arg Glu Met Gln Arg Glu Ile Leu Ser Ile Leu Gly Leu Pro His Arg
 47 55 60 65
 49 ccg cgc ccg cac ctc cag ggc aag cac aac tcg gca ccc atg ttc atg 297
 50 Pro Arg Pro His Leu Gln Gly Lys His Asn Ser Ala Pro Met Phe Met
 51 70 75 80
 53 ctg gac ctg tac aac gcc atg gcg gtg gag gag ggc ggc ggc ccc ggc 345
 54 Leu Asp Leu Tyr Asn Ala Met Ala Val Glu Glu Gly Gly Gly Pro Gly
 55 85 90 95
 57 ggc cag ggc ttc tcc tac ccc tac aag gcc gtc ttc agt acc cag ggc 393
 58 Gly Gln Gly Phe Ser Tyr Pro Tyr Lys Ala Val Phe Ser Thr Gln Gly
 59 100 105 110 115
 61 ccc cct ctg gcc agc ctg caa gat agc cat ttc ctc acc gac gcc gac 441
 62 Pro Pro Leu Ala Ser Leu Gln Asp Ser His Phe Leu Thr Asp Ala Asp
 63 120 125 130
 65 atg gtc atg agc ttc gtc aac ctc gtg gaa cat gac aag gaa ttc ttc 489
 66 Met Val Met Ser Phe Val Asn Leu Val Glu His Asp Lys Glu Phe Phe

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67          135          140          145
69 cac cca cgc tac cac cat cga gag ttc cgg ttt gat ctt tcc aag atc 537
70 His Pro Arg Tyr His His Arg Glu Phe Arg Phe Asp Leu Ser Lys Ile
71          150          155          160
73 cca gaa ggg gaa gct gtc acg gca gcc gaa ttc cgg atc tac aag gac 585
74 Pro Glu Gly Glu Ala Val Thr Ala Ala Glu Phe Arg Ile Tyr Lys Asp
75          165          170          175
77 tac atc cgg gaa cgc ttc gac aat gag acg ttc cgg atc agc gtt tat 633
78 Tyr Ile Arg Glu Arg Phe Asp Asn Glu Thr Phe Arg Ile Ser Val Tyr
79 180          185          190          195
81 cag gtg ctc cag gag cac ttg ggc agg gaa tcg gat ctc ttc ctg ctc 681
82 Gln Val Leu Gln Glu His Leu Gly Arg Glu Ser Asp Leu Phe Leu Leu
83          200          205          210
85 gac agc cgt acc ctc tgg gcc tcg gag gag ggc tgg ctg gtg ttt gac 729
86 Asp Ser Arg Thr Leu Trp Ala Ser Glu Glu Gly Trp Leu Val Phe Asp
87          215          220          225
89 atc aca gcc acc agc aac cac tgg gtg gtc aat ccg cgg cac aac ctg 777
90 Ile Thr Ala Thr Ser Asn His Trp Val Val Asn Pro Arg His Asn Leu
91          230          235          240
93 ggc ctg cag ctc tcg gtg gag acg ctg gat ggg cag agc atc aac ccc 825
94 Gly Leu Gln Leu Ser Val Glu Thr Leu Asp Gly Gln Ser Ile Asn Pro
95          245          250          255
97 aag ttg gcg ggc ctg att ggg cgg cac ggg ccc cag aac aag cag ccc 873
98 Lys Leu Ala Gly Leu Ile Gly Arg His Gly Pro Gln Asn Lys Gln Pro
99 260          265          270          275
101 ttc atg gtg gct ttc ttc aag gcc acg gag gtc cac ttc cgc agc atc 921
102 Phe Met Val Ala Phe Phe Lys Ala Thr Glu Val His Phe Arg Ser Ile
103          280          285          290
105 cgg tcc acg ggg agc aaa cag cgc agc cag aac cgc tcc aag acg ccc 969
106 Arg Ser Thr Gly Ser Lys Gln Arg Ser Gln Asn Arg Ser Lys Thr Pro
107          295          300          305
109 aag aac cag gaa gcc ctg cgg atg gcc aac gtg gca gag aac agc agc 1017
110 Lys Asn Gln Glu Ala Leu Arg Met Ala Asn Val Ala Glu Asn Ser Ser
111          310          315          320
113 agc gac cag agg cag gcc tgt aag aag cac gag ctg tat gtc agc ttc 1065
114 Ser Asp Gln Arg Gln Ala Cys Lys Lys His Glu Leu Tyr Val Ser Phe
115          325          330          335
117 cga gac ctg ggc tgg cag gac tgg atc atc gcg cct gaa ggc tac gcc 1113
118 Arg Asp Leu Gly Trp Gln Asp Trp Ile Ile Ala Pro Glu Gly Tyr Ala
119 340          345          350          355
121 gcc tac tac tgt gag ggg gag tgt gcc ttc cct ctg aac tcc tac atg 1161
122 Ala Tyr Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asn Ser Tyr Met
123          360          365          370
125 aac gcc acc aac cac gcc atc gtg cag acg ctg gtc cac ttc atc aac 1209
126 Asn Ala Thr Asn His Ala Ile Val Gln Thr Leu Val His Phe Ile Asn
127          375          380          385
129 ccg gaa acg gtg ccc aag ccc tgc tgt gcg ccc acg cag ctc aat gcc 1257
130 Pro Glu Thr Val Pro Lys Pro Cys Cys Ala Pro Thr Gln Leu Asn Ala
131          390          395          400

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133 atc tcc gtc ctc tac ttc gat gac agc tcc aac gtc atc ctg aag aaa 1305
134 ile Ser Val Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile Leu Lys Lys
135 405 410 415
137 tac aga aac atg gtg gtc cgg gcc tgt ggc tgc cac tagctcctcc 1351
138 Tyr Arg Asn Met Val Val Arg Ala Cys Gly Cys His
139 420 425 430
141 gagaattcag accctttggg gccaaagtttt tctggatcct ccattgctcg ccttggccag 1411
143 gaaccagcag accaactgcc ttttgtgaga ccttcccttc cctatcccca actttaaagg 1471
145 tgtgagagta ttaggaaaca tgagcagcat atggcttttg atcagttttt cagtggcagc 1531
147 atccaatgaa caagatccta caagctgtgc aggcataacc tagcaggaaa aaaaaacaac 1591
149 gcataaagaa aaatggccgg gccaggtcat tggctgggaa gtctcagcca tgcacggact 1651
151 cgtttccaga ggtaattatg agcgcctacc agccaggcca cccagccgtg ggagggaagg 1711
153 ggcgtggcaa ggggtgggca cattggtgtc tgtgcgaaag gaaaattgac ccggaagttc 1771
155 ctgtaataaa tgtcacaata aaacgaatga atgaaaaaaa aaaaaaaaaa a 1822
158 <210> SEQ ID NO: 2
159 <211> LENGTH: 431
160 <212> TYPE: PRT
161 <213> ORGANISM: Homo sapiens
163 <400> SEQUENCE: 2
164 Met His Val Arg Ser Leu Arg Ala Ala Ala Pro His Ser Phe Val Ala
165 1 5 10 15
167 Leu Trp Ala Pro Leu Phe Leu Leu Arg Ser Ala Leu Ala Asp Phe Ser
168 20 25 30
170 Leu Asp Asn Glu Val His Ser Ser Phe Ile His Arg Arg Leu Arg Ser
171 35 40 45
173 Gln Glu Arg Arg Glu Met Gln Arg Glu Ile Leu Ser Ile Leu Gly Leu
174 50 55 60
176 Pro His Arg Pro Arg Pro His Leu Gln Gly Lys His Asn Ser Ala Pro
177 65 70 75 80
179 Met Phe Met Leu Asp Leu Tyr Asn Ala Met Ala Val Glu Glu Gly Gly
180 85 90 95
182 Gly Pro Gly Gly Gln Gly Phe Ser Tyr Pro Tyr Lys Ala Val Phe Ser
183 100 105 110
185 Thr Gln Gly Pro Pro Leu Ala Ser Leu Gln Asp Ser His Phe Leu Thr
186 115 120 125
188 Asp Ala Asp Met Val Met Ser Phe Val Asn Leu Val Glu His Asp Lys
189 130 135 140
191 Glu Phe Phe His Pro Arg Tyr His His Arg Glu Phe Arg Phe Asp Leu
192 145 150 155 160
194 Ser Lys Ile Pro Glu Gly Glu Ala Val Thr Ala Ala Glu Phe Arg Ile
195 165 170 175
197 Tyr Lys Asp Tyr Ile Arg Glu Arg Phe Asp Asn Glu Thr Phe Arg Ile
198 180 185 190
200 Ser Val Tyr Gln Val Leu Gln Glu His Leu Gly Arg Glu Ser Asp Leu
201 195 200 205
203 Phe Leu Leu Asp Ser Arg Thr Leu Trp Ala Ser Glu Glu Gly Trp Leu
204 210 215 220
206 Val Phe Asp Ile Thr Ala Thr Ser Asn His Trp Val Val Asn Pro Arg
207 225 230 235 240

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```

209 His Asn Leu Gly Leu Gln Leu Ser Val Glu Thr Leu Asp Gly Gln Ser
210          245          250          255
212 Ile Asn Pro Lys Leu Ala Gly Leu Ile Gly Arg His Gly Pro Gln Asn
213          260          265          270
215 Lys Gln Pro Phe Met Val Ala Phe Phe Lys Ala Thr Glu Val His Phe
216          275          280          285
218 Arg Ser Ile Arg Ser Thr Gly Ser Lys Gln Arg Ser Gln Asn Arg Ser
219          290          295          300
221 Lys Thr Pro Lys Asn Gln Glu Ala Leu Arg Met Ala Asn Val Ala Glu
222 305          310          315          320
224 Asn Ser Ser Ser Asp Gln Arg Gln Ala Cys Lys Lys His Glu Leu Tyr
225          325          330          335
227 Val Ser Phe Arg Asp Leu Gly Trp Gln Asp Trp Ile Ile Ala Pro Glu
228          340          345          350
230 Gly Tyr Ala Ala Tyr Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asn
231          355          360          365
233 Ser Tyr Met Asn Ala Thr Asn His Ala Ile Val Gln Thr Leu Val His
234          370          375          380
236 Phe Ile Asn Pro Glu Thr Val Pro Lys Pro Cys Cys Ala Pro Thr Gln
237 385          390          395          400
239 Leu Asn Ala Ile Ser Val Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile
240          405          410          415
242 Leu Lys Lys Tyr Arg Asn Met Val Val Arg Ala Cys Gly Cys His
243          420          425          430
246 <210> SEQ ID NO: 3
247 <211> LENGTH: 102
248 <212> TYPE: PRT
249 <213> ORGANISM: Artificial Sequence
251 <220> FEATURE:
252 <223> OTHER INFORMATION: Description of Artificial Sequence: OPX
254 <220> FEATURE:
255 <221> NAME/KEY: VARIANT
256 <222> LOCATION: (1)..(102)
257 <223> OTHER INFORMATION: wherein each Xaa is independently selected from a
258 group of one or more specified amino acids as
259 defined in the specification
261 <400> SEQUENCE: 3
W--> 262 Cys Xaa Xaa His Glu Leu Tyr Val Ser Phe Xaa Asp Leu Gly Trp Xaa
263      1          5          10          15
W--> 265 Asp Trp Xaa Ile Ala Pro Xaa Gly Tyr Xaa Ala Tyr Tyr Cys Glu Gly
266      20          25          30
W--> 268 Glu Cys Xaa Phe Pro Leu Xaa Ser Xaa Met Asn Ala Thr Asn His Ala
269      35          40          45
W--> 271 Ile Xaa Gln Xaa Leu Val His Xaa Xaa Xaa Pro Xaa Xaa Val Pro Lys
272      50          55          60
W--> 274 Xaa Cys Cys Ala Pro Thr Xaa Leu Xaa Ala Xaa Ser Val Leu Tyr Xaa
275      65          70          75          80
W--> 277 Asp Xaa Ser Xaa Asn Val Ile Leu Xaa Lys Xaa Arg Asn Met Val Val
278      85          90          95

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Input Set : A:\Cbm-70wo.app
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W--> 280 Xaa Ala Cys Gly Cys His
      281           100
      284 <210> SEQ ID NO: 4
      285 <211> LENGTH: 97
      286 <212> TYPE: PRT
      287 <213> ORGANISM: Artificial Sequence
      289 <220> FEATURE:
      290 <223> OTHER INFORMATION: Description of Artificial Sequence: Generic
      291       Sequence 7
      293 <220> FEATURE:
      294 <221> NAME/KEY: VARIANT
      295 <222> LOCATION: (1)..(97)
      296 <223> OTHER INFORMATION: wherein each Xaa is independently selected from a
      297       group of one or more specified amino acids defined
      298       in the specification
      300 <400> SEQUENCE: 4
W--> 301 Leu Xaa Xaa Xaa Phe Xaa Xaa Xaa Gly Trp Xaa Xaa Trp Xaa Xaa Xaa
      302   1           5           10           15
W--> 304 Pro Xaa Xaa Xaa Xaa Ala Xaa Tyr Cys Xaa Gly Xaa Cys Xaa Xaa Pro
      305           20           25           30
W--> 307 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Asn His Ala Xaa Xaa Xaa Xaa Xaa
      308   35           40           45
W--> 310 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Cys Xaa Pro
      311   50           55           60
W--> 313 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Leu Xaa Xaa Xaa Xaa Xaa Xaa Xaa
      314   65           70           75           80
W--> 316 Val Xaa Leu Xaa Xaa Xaa Xaa Xaa Met Xaa Val Xaa Xaa Cys Xaa Cys
      317           85           90           95
W--> 319 Xaa
      323 <210> SEQ ID NO: 5
      324 <211> LENGTH: 102
      325 <212> TYPE: PRT
      326 <213> ORGANISM: Artificial Sequence
      328 <220> FEATURE:
      329 <223> OTHER INFORMATION: Description of Artificial Sequence: Generic
      330       Sequence 8
      332 <220> FEATURE:
      333 <221> NAME/KEY: VARIANT
      334 <222> LOCATION: (1)..
      335 <223> OTHER INFORMATION: wherein each Xaa is independently selected from a
      336       group of one or more specified amino acids defined
      337       in the specification
      339 <400> SEQUENCE: 5
W--> 340 Cys Xaa Xaa Xaa Xaa Leu Xaa Xaa Xaa Phe Xaa Xaa Xaa Gly Trp Xaa
      341   1           5           10           15
W--> 343 Xaa Xaa Xaa Xaa Xaa Pro Xaa Xaa Xaa Xaa Ala Xaa Tyr Cys Xaa Gly
      344           20           25           30
W--> 346 Xaa Cys Xaa Xaa Pro Xaa Xaa Xaa Xaa Xaa Xaa Xaa Asn His Ala
      347   35           40           45

```

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY

DATE: 09/26/2000

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Input Set : A:\Cbm-70wo.app

Output Set: N:\CRF3\09262000\I423943.raw

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:262 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:265 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:268 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:271 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:274 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:277 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:280 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:301 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:304 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:307 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:310 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:313 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:316 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:319 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:340 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:343 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:346 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:349 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:352 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:355 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:358 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:379 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:382 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:385 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:388 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:391 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:394 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:397 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:418 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:421 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:424 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:427 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:430 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:433 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:436 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:456 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:477 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9